AMENDMENTS TO THE CLAIMS

1. (Currently Amended) A method for characterising nucleic acid molecules, which comprises the steps of:

i) introducing a modified base which is a substrate for a DNA glycosylase into a DNA molecule;

ii) excising the modified base by means of said DNA glycosylase so as to generate an abasic site;

iii) cleaving the DNA at the abasic site so as to generate and release an extendible upstream DNA fragment having a 3′ hydroxyl terminus**, wherein the specificity of the extendible fragment is determined by the sequence of the target nucleic acid**; and

iv) incubating the released extendible upstream DNA fragment in the presence of an enzyme allowing for extension thereof and a template nucleic acid, which has partial or full sequence complementarity to the upstream fragment and analysing resultant fragment(s).

2. (Original) A method according to Claim 1, wherein the upstream fragment is generated by cleaving the DNA at the 5'side of the abasic site, such that the 3'terminus of the upstream fragment bears a hydroxyl group.

3. (Original) A method according to Claim 2, wherein the cleavage is achieved with a 5'AP endonuclease.

4. (Original) A method according to Claim 1, wherein the upstream fragment is generated by cleaving at the 5' side of the abasic site so as to leave a phosphate group at the 3'terminus of the upstream fragment and removing the phosphate group so that the upstream fragment bears a hydroxyl group at the 3'terminus.

5. (Original) A method according to Claim 1, wherein the upstream fragment is generated by cleaving at the 3'side of the abasic site so as to generate a deoxyribose phosphate group at the 3'terminus of the upstream fragment and subsequently removing the deoxyribose group to leave a hydroxyl group at the 3'terminus.

6. (Previously Presented) A method according to Claim 1, wherein 5' deoxyribose moieties downstream of the 3'terminus of the upstream fragment are removed so that the upstream fragment can be extended on the template.

7. (Original) A method according to Claim 6, wherein the

5'deoxyribose moieties are removed by a 5'deoxyribophosphodiesterase.

8. (Previously Presented) A method according to Claim 1, wherein the modified base is introduced by enzymatic amplification of the DNA.

9. (Original) A method according to Claim 8, wherein the amplified strands are separated for a separate analysis of the respective strands.

10. (Previously Presented) A method according to Claim 8, wherein a primer or one or more nucleotide (s) involved in the enzymatic amplification is labelled.

11. (Previously Presented) A method according to Claim 1, wherein the enzyme is a polymerase.

12. (Previously Presented) A method according to Claim 11, wherein the extendible upstream fragment is incubated in step iv) with the polymerase in the presence of one or more nucleotide (s).

13. (Original) A method according to Claim 12, wherein one or more of the nucloeotide (s) of step iv) is a dideoxy nucleotide.

14. (Previously Presented) A method according to Claim 12, wherein one or more of the nucleotide (s) of step iv) is labelled.

15. (Previously Presented) A method according to Claim 11, wherein the extension of step iv) is achieved by means of an amplification reaction using said extendible DNA fragment.

16. (Previously Presented) A method according to Claim 11, wherein the extension of step iv) is achieved by means of an amplification reaction including a primer in addition to using said extendible DNA fragment.

17. (Previously Presented) A method according to Claim 1, wherein the enzyme is a ligase.

18. (Original) A method according to Claim 17, wherein the extendible upstream fragment is incubated with the ligase in the presence of a reporter oligonucleotide.

19. (Original) A method according to Claim 18, wherein the reporter oligonucleotide is partially degenerate.

20. (Previously Presented) A method according to Claim 1, wherein any extended fragments resulting from step iv) are detected by hybridisation.

21. (Previously Presented) A method according to Claim 1, which is used to detect a known or unknown mutation.

22. (Cancelled)

23. (Previously Presented) A method according to Claim 1, wherein the method is used to analyse the CpG content of DNA by detecting C to T transitions in DNA.

24. (Cancelled)